Synchronous Balanced Analysis

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Overview

* What?

Piecewise synchronous approximation of Chemical Reaction Networks' (CRN) dynamics

* Mhys

- highlight interdependence of cellular processes
- finite cellular resource allocation VS cellular processes (i.e., growth)
- rephrase mass action run of CRNs as an optimisation problem

* Hows

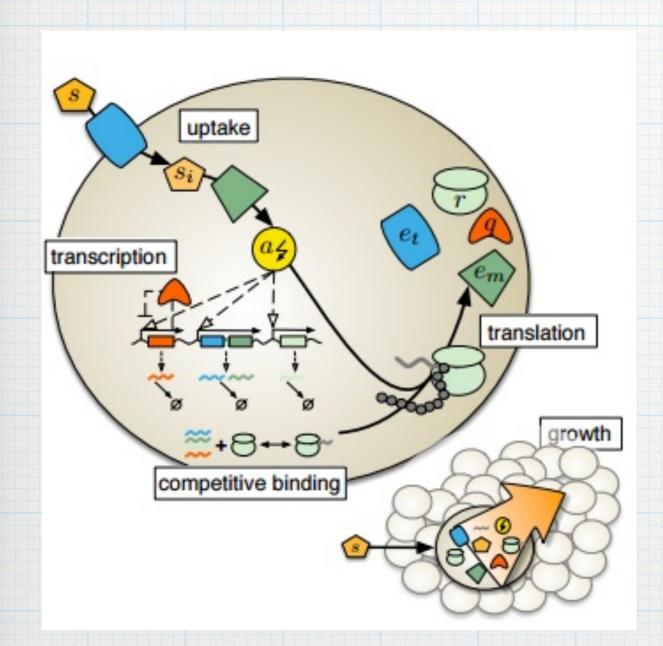
Resource allocation centred Petri Nets with maximal-step execution semantics

* Usage?

Approximation of real dynamics, constraint-based model similar to Flux Balance Analysis

Work in progress!

Motivation



Andrea Y. Weiße, Diego A. Oyarzún, Vincent Danos, and Peter S. Swain **Mechanistic links between cellular trade-offs, gene expression, and growth** PNAS 2015 112 (9) E1038-E1047; 2015, doi:10.1073/pnas.1416533112

Cellular processes rarely work in isolation: the rest of the cell cannot be ignored.

Finite cellular resources: committing to one task reduces the amount available to others

Define a formal notion of "growth": use as an improved biomass function in FBA

Modeling CRNs

 $CRN = \langle S, \nabla^+, \nabla^-, R, K \rangle$

PN = <P, T, W, mo >

species $\{S_1,\dots,S_s\}$

reactions $\{R_1, \ldots, R_r\}$

stoichiometry matrices

$$\nabla^{+} \in \mathbb{R}^{r \times s}$$
$$\nabla^{-} \in \mathbb{R}^{r \times s}$$

reaction rate constants

$$\kappa: R \to \mathbb{R}_{>0}$$

places

initial marking

 $m_0:P\to\mathbb{N}$

transitions

$$\forall s, t : \nabla^-(s, t) = W(s, t)$$

$$\forall s, t : \nabla^+(s, t) = W(t, s)$$

$$\nabla = \nabla^+ - \nabla^-$$

$$W: ((S \times T) \cup (T \times S)) \to \mathbb{N}$$

CRN mass action dynamics

reaction:

$$r_i: \sum_{j=1}^s \nabla_{ij}^- S_j \xrightarrow{k_i} \sum_{j=1}^s \nabla_{ij}^+ S_j$$

reaction network:

$$\nabla^- S \xrightarrow{k} \nabla^+ S$$

system state:

$$x = (x_{S_1}, ..., x_{S_s}) \in \mathbb{N}^s$$

CRN dynamics:

$$\frac{dx}{dt} = (\nabla^+ - \nabla^-)^T \cdot K \cdot x^{\nabla^-}$$

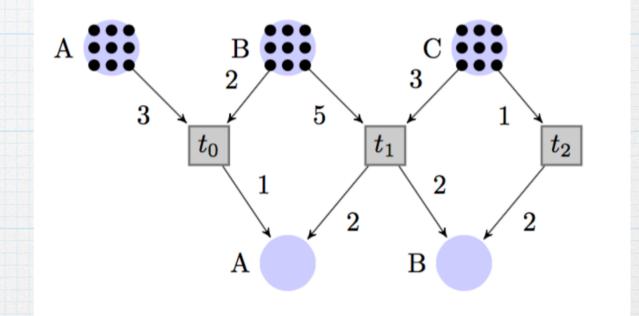
 $K = diag(\kappa_1, ..., \kappa_r)$ vector-matrix exponentiation

Petri Nets & Chemical Reaction Networks

$$3A + 2B \xrightarrow{\kappa_0} A$$

$$5B + 3C \xrightarrow{\kappa_1} 2A + 2B$$

$$C \xrightarrow{\kappa_2} 2B$$

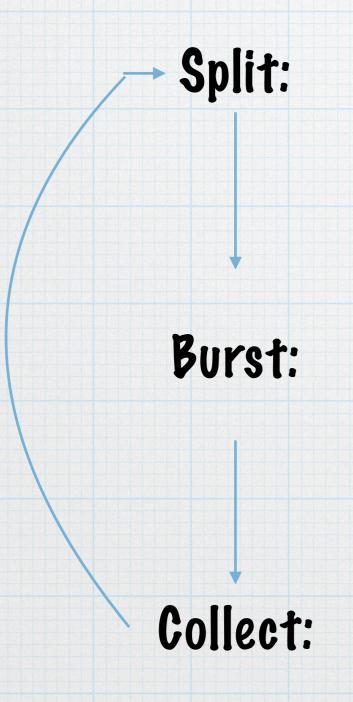


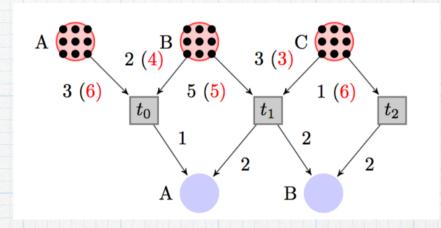
$$m_0 = (9, 9, 9)$$

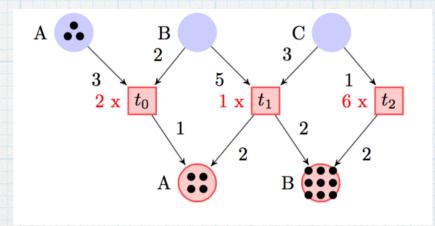
$$\nabla^{-} = \begin{bmatrix} 3 & 2 & 0 \\ 0 & 5 & 3 \\ 0 & 0 & 1 \end{bmatrix}$$

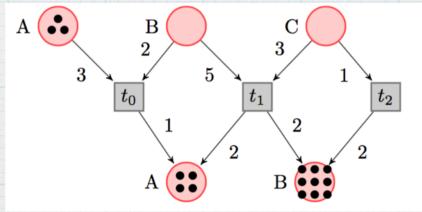
$$\nabla^{+} = \begin{bmatrix} 1 & 0 & 0 \\ 2 & 2 & 0 \\ 0 & 2 & 0 \end{bmatrix}$$

Piecewise synchronous execution









"SPLIT": resource allocation

reaction

Resource allocation matrix: α_{ij} _____ species

$$\alpha \in \mathbb{R}^{|T| \times |S|}$$

$$\forall j \in S, \sum_{i \in T} \alpha_{ij} \le 1$$

Interpretation: resource fraction VS reaction probability

"BURST": Max-parallel execution semantics of PN

"execute greedily as many transitions as possible in one step"

Definition:

A max-parallel execution step in a PN at state m is a positive T-vector v s.t.:

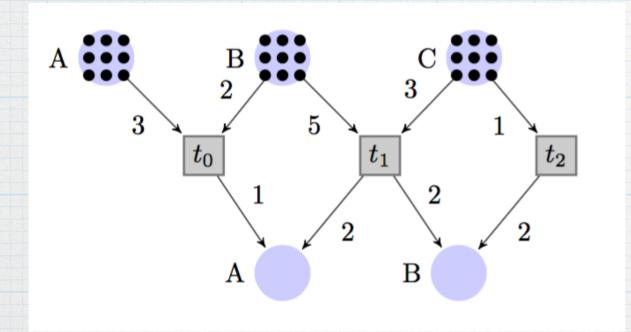
1. v is compatible with m:

$$0 \le m - \nabla^- v$$

2. v is exhaustive:

 $\forall j \in T, m - \nabla^- v \ngeq r_j$, where r_j is the j^{th} column of ∇^-

"BURST": Max-parallel execution semantics of PN



$$\{t_0 \times 3, t_2 \times 9\}$$

 $\{t_0 \times 2, t_1, t_2 \times 6\}$

Resource allocation & Max Parallel Execution

Define

$$(\alpha \star m)_j = \min_{i \in S} \left(\frac{\alpha_{ji}}{\nabla_{ij}^-} \cdot m_i\right)$$

Theorem:

 $\forall v$ compatible with a resource array m (and potentially max-parallel),

 $\exists \alpha$ resource allocation matrix s.t. $v = \alpha \star m$. Furthermore, if the CRN is unary, there is unicity of α

Our execution semantics encompasses max-parallel execution

Growth in unary CRNs

State of the system after 1 execution with given a split:

$$(I + \nabla \cdot \alpha) \cdot m$$

State of the system after k executions with given a split:

$$D_{\alpha}^{k} \cdot m$$
, with $D_{\alpha} = I + \nabla \cdot \alpha$

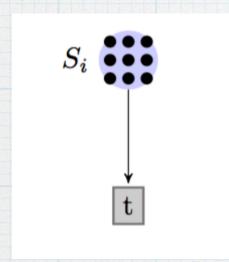
$$\lambda_1 > \lambda_2 > \cdots$$
, the eigenvalues of D_{α}

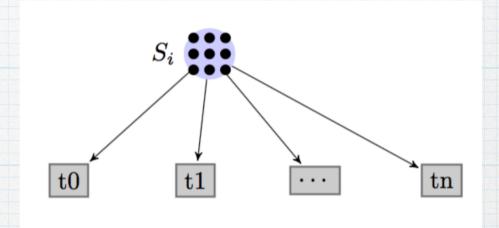
$$m = \sum_{i} m_{i}$$
, with $m_{i} \in E(\lambda_{i})$

$$D_{\alpha}^{k} \cdot m = \lambda_{1}^{k} \cdot \left[m_{1} + \sum_{i \geq 2} \left(\frac{\lambda_{i}}{\lambda_{1}} \right)^{k} \cdot m_{i} \right]$$

The growth rate of the system is given by λ_1 .

Unary CRNs and Depletion Time





$$S_i \to \dots @k$$

$$\tau = k^{-1} \log(\frac{S_i(0)}{s_i})$$

$$S_i \to \dots @k_j; j \in N_i, |N_i| = n$$

$$\tau_j = k_j^{-1} \cdot \log(\alpha_{ji} \cdot \frac{S_i(0)}{S_{i,j}})$$

depletion level

Unary CRNs: "iso" assumptions

Decouple production and consumption

Isochronous:

$$\forall j \in N_i, \tau_j = \tau$$

Iso-remainder:

$$\forall j \in N_i, s_{i,j} = s_i$$

$$\Delta m(\tau) = \nabla \cdot (\alpha_{-i} - \epsilon_{-i}) \cdot m$$

$$\frac{\Delta m}{\tau} \approx^{\tau \to 0} \nabla \cdot [k_j] \cdot m$$

The usual ODE dynamics is recreated:
$$\frac{dx}{dt} = (\nabla^+ - \nabla^-)^T \cdot K \cdot x^{\nabla^-}$$

Unary CRNs: "iso" assumptions

$$\hat{\alpha}_{S_i}(\tau, \hat{k_{S_i}}) = \left[\alpha_{-i} - \epsilon_{-i}\right] = \left[\frac{e^{\tau \cdot k_j} - 1}{\sum_{j} 1 + e^{\tau \cdot k_j}}\right]$$

Resource allocation matrix as a function of depletion time and reaction rate constants!

Concrete interpretation

Approximation of system dynamics:

- temporised discrete execution
- "don't wait for the slowest reaction"
- simulation: big step approx. of an integrator (deterministic tau-leaping)

Abstract interpretation

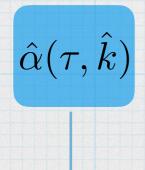
Synchronous Balanced Analysis

Objective function: λ_1

$$D_{\alpha}^{k} \cdot m = \lambda_{1}^{k} \cdot [m_{1} + \sum_{i \geq 2} (\frac{\lambda_{i}}{\lambda_{1}})^{k} \cdot m_{i}]$$



amax



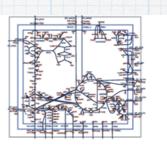
a Genome-scale metabolic reconstruction



Mathematically represent metabolic reactions and constraints



Mass balance defines a system of linear equations

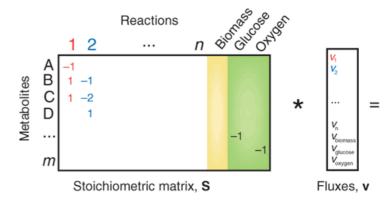


 $A \longleftrightarrow B + C$ $B + 2C \longrightarrow D$

Reaction 1
Reaction 2

•••

Reaction n



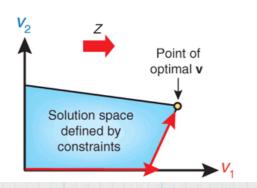
$$-V_1 + ... = 0$$

 $V_1 - V_2 + ... = 0$
 $V_1 - 2V_2 + ... = 0$
 $V_2 + ... = 0$
etc.

Define objective function $(z = c_1^* v_1 + c_2^* v_2 \dots)$

To predict growth, $Z = v_{\text{biomass}}$

Calculate fluxes that maximize Z



SBA VS.FBA

- · able to handle growth (no steady state assumption needed)
- take into account real system kinetics
- characterise behaviour of a cell using only one construction: α
- · replace mechanistic details of resource allocation with an abstract vector
- · objective biomass function emerges directly from method: growth rate
- · maximising biggest eigenvalue of matrix: how?

Future work

- binary reactions: depletion time? (Michaelis-Menten type assumption)
- explore correlations between growth rate and model parameters
- · tau-leaping, whole-cell models by Karr, etc...

Conclusion

Piecewise synchronous approximation of the dynamics of (growth) CRNs:

parallel execution semantics of PN, based on resource allocation.

Interpretations:

l. approx. of real system dynamics constraint based method (like FBA)

Thank you!